

Amendments to the claims:

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified Avill peptide with cellulase activity and, said Avill peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme having at least 70 90% identity to SEQ ID NO. 1, said Avill peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (Avill_Aac).

GH74_Aac	NFTDQPTWAVNVLCCCCFVDCIVPNECAPCGILYVRTTDCCGMYRNDANCRWIPILLDWG
Avi74_Aac	AASQAYTNKAVATGGCGCPTCIVPNSAAGCVAVARYRTDCCAYRINSDDWTWPLMDWVG
GH74_Aac	WNNHCGVAGCAGTAAADPNTWVWVHAAVCMYTFNSNDPNDGATLRS68POCATWQITPLDEKLG
Avi74_Aac	NTSHWDWGIDALMTDPVDTDRIVVAVCMYTFNENDENVCGTILRS68DQSTWTSIGLEPKHG
GH74_Aac	CNMPGRCMGBALAVDPNNVSLVLYFCARSKXCLWRKSTDCCATWQMTNFPDVCTYIANPTD
Avi74_Aac	CNMPGRCMGERALAVDPNNVSLVLYFCARSKXCLWRKSTDCCATWQMTNFPDVCTYFQDSSZ
GH74_Aac	TRGYQ8DIQGIVWVAPDKS888LQGAS6XTKTFVCAVADPNNPVPVWSRDCCATWQAVPCAP-T
Avi74_Aac	T-VTSDPVGIAWTFDSTEGEGSATPRIFVCAVADACKCIVFKSEDCAGATWAVVEGEPQY
GH74_Aac	GFLPKKGVLSPPEKTLIYIYANGACPYDGTNTVHICWVITSGCWTBISP-TSLASTPV
Avi74_Aac	GFLPKKGVLSPPEKTLIYIYANGACPYDGTNTVHICWVITSGCWTBISP-TSLASTPV
GH74_Aac	GYCGGLTIDRQHNTTINVATOTWNPDTTIFRSTDGGATWTRIWBWTOVNPRLRFLYDIX
Avi74_Aac	GYCGGLSVBLOVPTGLMVANLNCWNPDELLIFRSTDGGATWSPINHNGPSINPFLYDIX
GH74_Aac	AEPWVITFCVQPNPPTVCPKLGWDEAMALDPPNQDRWVYCTGATLVAITNDLTWDGCGQI
Avi74_Aac	NAPWQDITTSCTDQP-VRVQHIVTEALAIADPFDNSHAWVCTGCLTIVZCHDLTWDGCGQI
GH74_Aac	HIAFWVKGCLPDTAVWPLICPPCCAPLTCALGDLGGFWWDVTAUTCTIFTCPVFTTCTV
Avi74_Aac	TVKGLAVGDTAVWPLICPPCCAPLTCALGDLGGFWWDVTAUTCTIFTCPVFTTCTV
GH74_Aac	DYAEIINPCITVAGCFFDPCGQPVDRIVAFCTBGGFWWDVGGCFTCTVAAACADCCR
Avi74_Aac	DYAGAKKPCITVAGCFFDPCGQPVDRIVAFCTBGGFWWDVGGCFTCTVAAACADCCR

GH74_Aee	PWAPCDPGDPVPPVAVPGFGNSWANACQCPVPAQIQRGDRVNPFTFVNLNQCTFYRSTDCCV
Avilll_Aee	VLLMGGTSGALVXGQQ
GH74_Aee	TQDPDVAACLPLSSCAVGVMPHAWPCKSCDLWLAASSGLYHGTNGGGSWAL
Avilll_Aee	CPTKTKVG LGGCTTVNAAIR AWPSTACDVAESTDKLWHSTDVCSTPQICSGCVTTAGWCF
GH74_Aee	CPCKKAAPC88VAVVIVVWTCGCVTAATCDDDCGTTWVLENDQEVCN WCGATTCGKAN
Avilll_Aee	CPCKKAATC88VAVVIVCATTIDCAGVNLWKGDTWVQGACTGPFCCGATVWNGDQF
GH74_Aee	LRRPVFGTNGRGRVPPVPPGPPS
Avilll_Aee	VGRVPRGHTPGLRGGGSPAG

2. (Previously Presented) The composition of claim 1 wherein the Avilll peptide is further defined as comprising a linker and a signal sequence.

3. (Cancelled)

4. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilll peptide is further defined as comprising a length of about 80 to about 150 amino acids.

5. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the Avilll peptide is further defined as comprising a length of about 90 amino acids.

6. (Previously Presented) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.

7. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Previously Presented) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Previously Presented) The composition of claim 1 wherein said Avilll protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74_Ace has at least 90% sequence identity with SEQ ID NO: 3.

11. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.

12. (Previously Presented) An isolated Avill peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Presented) An industrial mixture suitable for degrading cellulose, such mixture comprising the Avill polypeptide of claim 1.

15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[]

16-27 (Cancelled)

28. (Previously Presented) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;
- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Presented) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (New) The composition of claim 1 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII_Aac):

GH74_Ace ATTQPYTWSNVIAGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAAANGRWIPLLDDWVG
AvIII_Aac AASQAYTWNVNTGGGGGFTPQIVFVNPSAKGVAYARTDIGGAYRLNSDD-TWIPPLMDWVG

GH74_Ace
AvIII_Aac
WNNWGYGVVSIADPINTNKWAAVGMYTNWDPMGDAILRSSDQGATWQITPLPFKLG
NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPMVGSIILRSSTDQGDTWETKLFVFGV

GH74_Ace
AVIII_AAC

GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLNRSTDGATWSQMTNFPDVGTYLANPTD
GNMPGRGMGERLAVDPNKNSLILYFGARSGHGLWKSTDYGAWSNVTSPTWGTYFQDSSS

GH74_Ace TTGYQSIDIQGVVVAPDKSSSSLGQASKTIFVGVDAPNNPVPWSRDGGATWQAVPGAP-TT
AvIII_Aac T- -YTSDFVGIANVTFDSTSGSSGSATPRIFVGVDAGKSFKSEDAGATWAWVSGEEQY

GH74_Ace GFIPHKGVFDPVNHLVLYIATSNTPGYPDGSSGDVWKFSVTGWTWRISPVPSTDTANDYP
AvIII_Aac GPLPHKGVLSPESKTLVYISYANGAGPYDGTGNTVHKYNIITSGVWTDISP---TSLASTYY

GH74_Ace	GYSGLTIDRQNPNTIMVATQISWWPDITIIPRSTDGGATWTRIWDTSYPNRSLRYVLDIS
AviIII_Aac	GYGGLSVDLQVPGTLMAALNCWWPDELIFRSTDGATWSPIWENNGYPSINYYSYDIS ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	AEPWLTFGVQPNPPVPSPKLGMDEAMAIDPFNSDRMLYGTGATLYATNDLTWDGSGQI
AviIII_Aac	NAPWQDITSTDQFP--VRVGWMVLAIDPFDSNHLYGIGLTIVYGGHDLITWDGSKHNV ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTADVTAVPSTIFTSPVPTTGTSV
AviIII_Aac	TVKSLAVGIEEAVLGLITPPCGPALLSAVGDDGCFYHSDLAAAPNQAYHTPTYGTNTGI ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	DYAEINPSIIVRAGSFDPSQPNDRHVAFTDGGKKNWFQGSEPGGVTTGGTVAA\$ADGSR
AviIII_Aac	DYAGNPKPSNIVRSGASDDYP----TLALSSNPGSTWYADYAASTSTGTGAVALSADGDT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	FVWAPGDPGQPVYAVGFGNSWAASQGVPNANAQIRSDKVNPKTFYALSGNTFYRSTDGGV
AviIII_Aac	VLLMSSTSGALVSKSQG---TITA VSSLPSGAVIAGDKSDNTVFPYGGSAGAIYVSKDTAT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	TFQFVAAGLPSSGAVGVMFHAVPGKEGDLWLAAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac	SFTKTIVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTPTQIGSGVTAGWSF ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	GFGKSAPGSSYPAVFVVGTTIGGVIGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac	GFGKASSTGSYVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVNGDLQT ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac	YGRVFRGHERPGHLLRQSQRREPAG ***:***:***:***:***:***

48. (New) The composition of claim 47 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (New) A composition comprising a substantially purified AviIII peptide having at least 99% identity to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (New) The composition of claim 49 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII_Aac):

GH74_Ace	ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVVRTDIGGMYRWDAAANGWIPLLDWVG
AviIII_Aac	AASQAYTWWKVVVTGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	WNNWGYNGVVSIAADPINTNKVAAVGMYTNSWDPNDDGATLRSQDQGATWQITPLPPKLG
AviIII_Aac	NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWETKLPFKVG ***:***:***:***:***:***:***:***:***:***:***:***:***:***:***:***
GH74_Ace	GNMPGRGMGERLAVDPNNNDNLYFGAPSGKGLWRSTDGATWSQMTNFPDVGTYIANPTD
AviIII_Aac	GNMPGRGMGERLAVDPNKNNSILYFGARSGHGLWKSTDYGATW3NVTSTWTGTYFQDSS9 *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****

GH74_Ace	TTGYQSDIQGVVVVAFDKSSSSLGQASKTIFVGVADPNNPVPWSRDGGATWQAVPGAP-T
AviIII_Aac	T--YT\$DPVGLAWVTFDSTSGSSGSAATRIFVGVADAGKSVFKSEDAGATWAWVSGBPQY * * * * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	GFIPIHKGVFDPPVNMVLYIATSGTGGFYDGSSGDVWKPSVTSGTWRISPVPSSTDNTANDYF
AviIII_Aac	GFLPHKGVLSPPEKTLIYISYANGAGPYDGTNGTVHKNITSGVMTDISP---TSLASTYY * * ; * * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	GYSGLTIDROHPNTIMVATQISWNPDIIIFRSTDGGATWTRIWDWTSPNRSIRYVLDIS
AviIII_Aac	GYGGLSVDLQVPGTLMVAALNCWNPDELIIFRSTDGGATWSPIEWNGPSINYYYSYDIS * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	AEPWLTFGVQPNNPPVPSPKLGWMDEAIDPPNSDRMLYGTGATLYATNDLTWDSDGGQI
AviIII_Aac	NAPWIQDTTSTDQFP--VRVGMWVLEALIDPFDSHMLYGTGLTVYGGHDLTNWDSIGHNV * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	HIAPMVKGLEETAVNDLISPPSCAPLISALGDLGGFTHDADVTPSTIFTSPVFTTGTSV
AviIII_Aac	TVKSLAVGIEEMAVLGLITPPGGFALLSAVGDDGGFYHSDLDAAPNQAYHTPYGTINIG * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	DYARLNP\$IIIVRAGSFDPSSQPNDRHVAFSTDGGKRNWFQGSEPGGVITCGTVAAASADGSR
AviIII_Aac	DYAGNKP\$NIIVRSGASDDYP---TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	FVWAPGDPGOPVYAVGFGNSWAASQGV PANQIRSDRVNPKTFYALSGNTPYRSTDGGV
AviIII_Aac	VJLMSSSTS GALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVYGGSAGAIYVSKNTAT * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	TFQPVAAGLPSGAVGVMPHAVPGKEGLWLAA\$GLYH\$TNGSSWSAI-TGVSSAVNV
AviIII_Aac	SPTKTVS-LGSSTTVNAIR-AHPSIAGDVWA\$TDKGLWH\$TDYGSTFTQIGSGVTAGNSF * * ; * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	GFGKSA\$PGSSYPAVFVUGTIGGVIGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac	GMGKASSTG\$YVVIYGGFTIDGAACLFKSEDAGTNWQVISDASHGFGSGSANVNGDLQT * * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ; * ;
GH74_Ace	LRRVYIGTNGRGIIVYGDIGGAPSG
AviIII_Aac	YGRVFRGHERPGHLLRQSREPAQ * * ; * ; * ; * ; * ;

51. (New) The composition of claim 50 wherein said AviIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (New) A composition comprising a substantially purified AviIII peptide having an amino acid sequence identical to SEQ ID NO. 1, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (New) A composition comprising a substantially purified AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

54. (New) The composition of claim 51 wherein said catalytic domain
GH74_Ace has a sequence identical to SEQ ID NO. 3.